

Figure 1A

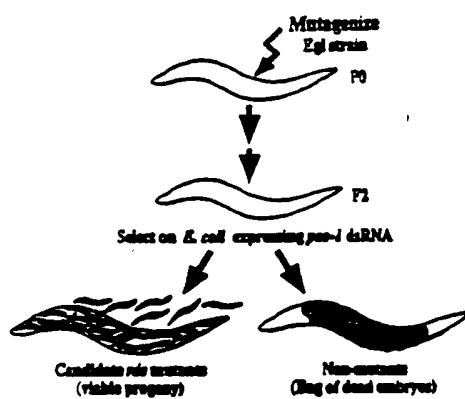


Figure 1B

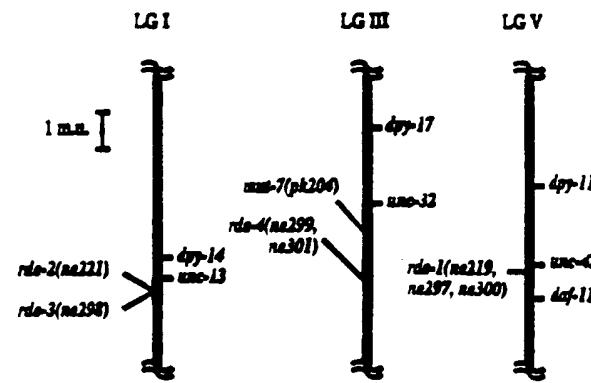


Figure 2

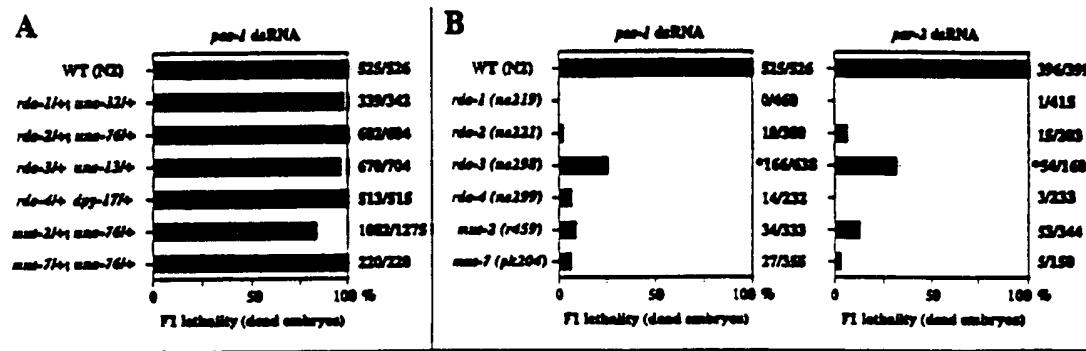


Figure 3

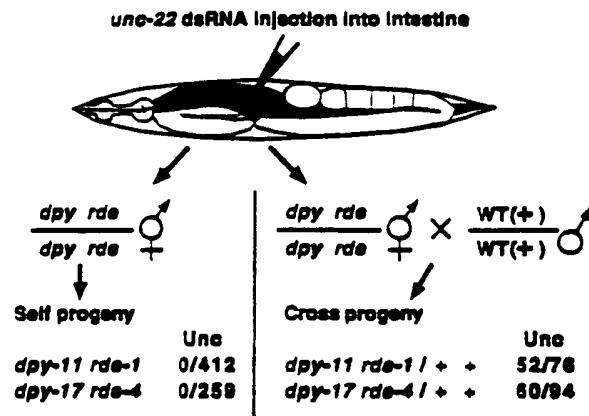
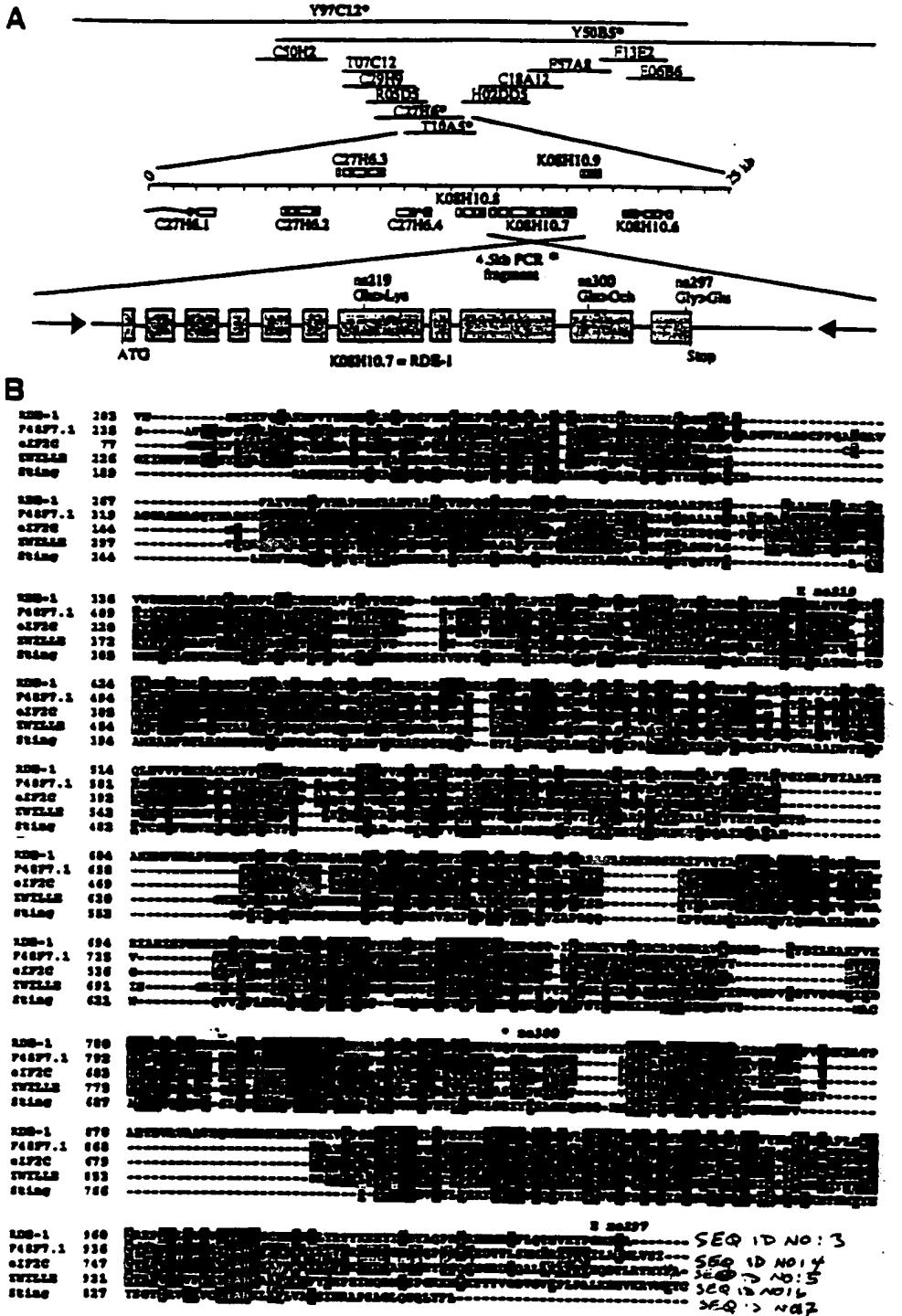


Figure 4



cagccacaaagtgatgaaacatgtcctcgaaatttcccgaaattggaaaaaggattttatcgtaattctcgatccggtagatcaattattagcagctataagatatataagttgatattaatattataggagatgaaatggcttgcgaggcccacttgtaaatgcgacggcaaattctatgagaagaaagtacttctttggtaattggttcaagttctccagcaaaattacatcggaataactacgagtgaaatgacaaggaaagtattgaatagaaaaccaggaaaaccttccaaaaaaagagaaattccaatgtaaatgtcgttgcatttttgcgtccgcgtcaacttttcgcgttgcgtcaactttctggcacatcttcggcatgagaagaaggcagacagatttattctcgaaagactatgttttgcgttgcgttgcactgtcacatcaaaaatgtcggttcggagaaagtagtagaaaaaggattcgagaaaaagatgaaaggattggagaaaaaatcttatacacaatgataacttacctatcgtaaaaaattcacctgaacttttagtcgagaaaatccggaaaaagacgaagaagcgaatcggagttacaattctcgaaaggttatgaaaaacacgcattataacaaacaaattagcttcagaatgttatgacccagaaagttcgctacgcgcctttgtgaacgaggagattaaagtgtgagttgcataataataataataatcacctcaactcatttatatttaagacaattcgcaaaaaatttgcgtacgataataattcaat

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Figure 5C

taaactttcagaacaacgacaatcgagcaccagcgcatattgttagtctatcgagacggagttacgattcgaggatgcata
cgtttagtcatgatgagctcgatctttaaaaagcgaagtaaaacaattcatgtcggaacggatggagaagatccaga
gccgaagtacacgttcattgtgattcagaaaagacacaatacacgattgtcgatgtttaaacaatggaggatgtgaaagaaac
tcaataaagatcttactcctgtgaaacagatgtcgctgtgtttaaacaatggaggatgtgaaagaaac
aaagaaaactggaattgtgaacccatcatcggaacaactgtggataaacttatcgttcgaaatacaaattcgattttt
cttgcacatctcatcatggtgtccttgtacatctcgccaggacattacactgttatgtatgacgataaaggaatgagcc
aagatgaagtctatgtaaacgtttttgaatagcagttacgtcgattttaggatttgtaatccgcatatagttattataaaaa
aatgtttcagaaaatgacacctacggacttgccttctctgttagatgtcgaaaacccatctgcgtgcctgtccgggttc
attatgctcatttatcatgtgaaaaagcgaaagagcttacgtaaactacgtgaagtaccctggatgtcgatgcataacatttgc
ccacggactcgacacgaaatggAACATTCTCCAAACTAACGTGAAGTACCGTGGATGTGTTGCATAACATTTC
aaaagtgtcgcccgttcaatcaaattttcaattgttagatattgtacttactttttaaagcccggttcaaaaatt
cattccatgactaacgtttcataaattacttgaaattt (SEQ ID NO: 1)

0580922 1001300

Figure 6A

CGGCCACAAAGTGTGAAAC- 3' UTR

1/1

31/11

ATG TCC TCG AAT TTT CCC GAA TTG GAA AAA GGA TTT TAT CGT CAT TCT CTC GAT CCG GAG
Met ser ser asn phe pro glu leu glu lys gly phe tyr arg his ser leu asp pro glu

61/21

91/31

ATG AAA TGG CTT GCG AGG CCC ACT GGT AAA TGC GAC GGC AAA TTC TAT GAG AAG AAA GTA
met lys trp leu ala arg pro thr glu lys cys asp glu lys phe tyr glu lys val

121/41

151/51

CTT CTT TTG GTA AAT TGG TTC AAG TTC TCC AGC AAA ATT TAC GAT CGG GAA TAC TAC GAG
leu leu leu val asn trp phe ser ser lys ile tyr asp arg glu tyr tyr glu

181/61

211/71

TAT GAA GTG AAA ATG ACA AAG GAA GTG AAT AGA AAA CCA GGA AAA CCT TTC CCA AAA
tyr glu val lys met thr lys glu val leu asn arg lys pro glu lys pro phe pro lys

241/81

271/91

AAG ACA GAA ATT CCA ATT CCC GAT CGT GCA AAA CTC TTC TGG CAA CAT CTT CGG CAT GAG
lys thr glu ile pro pro asp arg ala lys leu phe trp glu his leu arg his glu

301/101

331/111

AAG AAG CAG ACA GAT TTT ATT CTC GAA GAC TAT GTT TTT GAT GAA AAG GAC ACT GTT TAT
lys lys glu thr asp phe ile leu glu asp tyr val phe glu lys asp thr val tyr

361/121

391/131

AGT GTT TGT CGA CTG AAC ACT GTC ACA TCA AAA ATG CTG GTT TCG GAG AAA GTA GTA AAA
ser val cys arg leu asn thr val ser lys met leu val ser glu lys val val lys

421/141

451/151

AAG GAT TCG GAG AAA AAA GAT GAA AAG GAT TTG GAG AAA AAA ATC TTA TAC ACA ATG ATA
lys asp ser glu lys lys asp glu lys asp leu glu lys lys ile leu tyr thr met ile

481/161

511/171

CTT ACC TAT CGT AAA AAA TTT CAC CTG AAC TTT AGT CGA GAA AAT CCG GAA AAA GAC GAA
leu thr tyr arg lys lys phe his leu asn phe ser arg glu asn pro glu lys asp glu

541/181

571/191

GAA GCG AAT CGG AGT TAC AAA TTC CTG AAG AAT GTT ATG ACC CAG AAA GTT CGC TAC GCG
glu ala asn arg ser tyr lys phe leu lys asn val met thr glu lys val arg tyr ala

601/201

631/211

CCT TTT GTG AAC GAG GAG ATT AAA GTA CAA TTC GCG AAA AAT TTT GTG TAC GAT AAT AAT
pro phe val asn glu glu ile lys val glu phe ala lys asn phe val tyr asp asn asn

661/221

691/231

TCA ATT CTG CGA GTT CCT GAA TCG TTT CAC GAT CCA AAC AGA TTC GAA CAA TCA TTA GAA
ser ile leu arg val pro glu ser phe his asp pro asn arg phe glu glu ser leu glu

721/241

751/251

Figure 40

371/261	811/271
GGT GAA CCT GTG CTC AAT TTT GCA ATT GTC GAT AAA CTA TTC TAC AAT GCA CGG AAA ATG gly giu pro val leu asn phe ala ile val asp lys ieu phe tyr asn ala pro lys met	
341/281	871/291
TCT CTT CTG GAT TAT CTT CTC CTA ATT GTC GAC CCC CAG TCG TGT AAC GAT GAT GTA CGA ser leu leu asp tyr leu leu ile val asp pro gin ser cys asn asp asp val arg	
301/301	931/311
AAA GAT CTT AAA ACA AAA CTG ATG GCG GGA AAA ATG ACA ATC AGA CAA GCC GCG CGG CCA lys asp leu lys thr lys leu met ala gly lys met thr ile arg gin ala ala arg pro	
361/321	991/331
AGA ATT CGA CAA TTA TTG GAA AAT TTG AAG CTG AAA TGC GCA GAA GTT TGG GAT AAC GAA arg ile arg gin leu leu glu asn ieu lys leu lys cys ala giu val trp asp asn glu	
1021/341	1051/351
ATG TCG AGA TTG ACA GAA CGA CAT CTG ACA TTT CTA GAT TTG TGC GAG GAA AAC TCT CTT met ser arg leu thr giu arg his leu thr phe leu asp leu cys glu giu asn ser leu	
1081/361	1111/371
GTT TAT AAA GTC ACT GGT AAA TCG GAC AGA GGA AGA AAT GCA AAA AAG TAC GAT ACT ACA val tyr lys val thr giy lys ser asp arg gly arg asn ala lys lys tyr asp thr thr	
1141/381	1171/391
TTG TTC AAA ATC TAT GAG GAA AAC AAA AAG TTC ATT GAG TTT CCC CAC CTA CCA CTA GTC leu phe lys ile tyr glu glu asn lys lys phe ile glu phe pro his leu pro leu val	
1201/401	1231/411
AAA GTT AAA AGT GGA GCA AAA GAA TAC GCT GTA CCA ATG GAA CAT CTT GAA GTT CAT GAG lys val lys ser gly ala lys glu tyr ala val pro met glu his leu glu val his glu	
1261/421	1291/431
AAG CCA CAA AGA TAC AAG AAT CGA ATT GAT CTG GTG ATG CAA GAC AAG TTT CTA AAG CGA lys pro gin arg tyr lys asn arg ile asp leu val met gin asp lys phe leu lys arg	
1321/441	1351/451
GCT ACA CGA AAA CCT CAC GAC TAC AAA GAA AAT ACC CTA AAA ATG CTG AAA GAA TTG GAT sia thr arg lys pro his asp tyr lys glu asn thr leu lys met leu lys glu leu asp	
1381/461	1411/471
TTC TCT TCT GAA GAG CTA AAT TTT GTT GAA AGA TTT GGA TTA TGC TCC AAA CTT CAG ATG phe ser ser glu giu leu asn phe val glu arg phe giy leu cys ser lys leu gin met	
1441/481	1471/491
ATC GAA TGT CCA GGA AAG GTT TTG AAA GAG CCA ATG CTT GTG AAT AGT GTA AAT GAA CAA ile glu cys pro giy lys val leu lys giu pro met leu val asn ser val asn glu gin	
1501/501	1531/511
ATT AAA ATG ACA CCA GTG ATT CGT GGA TTT CAA GAA AAA CAA TTG AAT GTG GTT CCC GAA ile lys met thr pro val ile arg giy phe gin glu lys gin leu asn val val pro glu	

1561/521 1691/
AAA GAA CCT Ile TGT GCT CTT GTC AAC GAA ACA GCG GGA AAT CCA TGC TTA GAA
lys glu leu cys cys ala val phe val val asn glu thr ala gly asn pro cys leu glu

1621/541 1651/551
GAG AAC GAC GTT GTT AAG TTC TAC ACC GAA CTA ATT GGT GGT TGC AAG TTC CGT GGA ATA
glu asn asp val val lys phe tyr thr glu leu ile gly gly cys lys phe arg gly ile

1681/561 1711/571
CGA ATT GGT GCC AAT GAA AAC AGA GGA GCG CAA TCT ATT ATG TAC GAC GCG ACG AAA AAT
arg ile gly ala asn glu asn arg gly ala gln ser ile met tyr asp ala thr lys asn

1741/581 1771/591
GAA TAT GCC TTC TAC AAA AAT TGT ACA CTA AAT ACC GGA ATC GGT AGA TTT GAA ATA GCC
glu tyr ala phe tyr lys asn cys thr leu asn thr gly ile gly arg phe glu ile ala

1801/601 1831/611
GCA ACA GAA GCG AAG AAT ATG TTT GAA CGT CTT CCC GAT AAA GAA CAA AAA GTC TTA ATG
ala thr glu ala lys asn met phe glu arg leu pro asp lys glu gln lys val leu met

1861/621 1891/631
TTC ATT ATC ATT TCC AAA CGA CAA CTG AAT GCT TAC GGT TTT GTG AAA CAT TAT TGC GAT
phe ile ile ile ser lys arg gln leu asn ala tyr gly phe val lys his tyr cys asp

1921/641 1951/651
CAC ACC ATC GGT GTA GCT AAT CAG CAT ATT ACT TCT GAA ACA GTC ACA AAA GCT TTG GCA
his thr ile gly val ala asn gln his ile thr ser glu thr val thr lys ala leu ala

1981/661 2011/671
TCA CTA AGG CAC GAG AAA GGA TCA AAA CGA ATT TTC TAT CAA ATT GCA TTG AAA ATC AAC
ser leu arg his glu lys gly ser lys arg ile phe tyr gln ile ala leu lys ile asn

2041/681 2071/691
GCG AAA TTA GGA GGT ATT AAC CAG GAG CTT GAC TGG TCA GAA ATT GCA GAA ATA TCA CCA
ala lys leu gly gly ile asn gln glu leu asp trp ser glu ile ala glu ile ser pro

2101/701 2131/711
GAA GAA AAA GAA AGA CGG AAA ACA ATG CCA TTA ACT ATG TAT GTT GGA ATT GAT GTA ACT
glu glu lys glu arg arg lys thr met pro leu thr met tyr val gly ile asp val thr

2161/721 2191/731
CAT CCA ACC TCC TAG AGT GGA ATT GAT TAT TCT ATA GCG GCT GTA GTA GCG AGT ATC AAT
his pro thr ser tyr ser gly ile asp tyr ser ile ala ala val val ala ser ile asn

2221/741 2251/751
CCA GGT GGA ACT ATC TAT CGA AAT ATG ATT GTG ACT CAA GAA GAA TGT CGT CCC GGT GAG
pro gly gly thr ile tyr arg asn met ile val thr gln glu glu cys arg pro gly glu

2281/761 2311/771
CGT GCA GTG GCT CAT GGA CGG GAA AGA ACA GAT ATT TTG GAA GCA AAG TTC GTG AAA TTG
arg ala val ala his gly arg glu arg thr asp ile leu glu ala lys phe val lys leu

2341/781 2371/791
CTC AGA GAA TTC GCA GAA AAC AAC GAC AAT CGA GCA CCA GCG CAT ATT GTA GTC TAT CGA
leu arg glu phe ala glu asn asn asp asn arg ala pro ala his ile val val tyr arg

1401/801 2431/11
GAC GGA GTT AGC GAT TCG GAG ATG CTA CGT GTT AGT CAT GAT GAG CTT CGA TCT TTA AAA
asp gly val ser asp ser glu met leu arg val ser his asp glu leu arg ser leu lys

2461/821 2491/831
AGC GAA GTA AAA CAA TTC ATG TCG GAA CGG GAT GGA GAA GAT CCA GAG CCG AAG TAC ACG
ser glu val lys gin phe met ser glu arg asp gly glu asp pro glu pro lys tyr thr
2521/841 2551/851
TTC ATT GTG ATT CAG AAA AGA CAC AAT ACA CGA TTG CTT CGA AGA ATG GAA AAA GAT AAG
phe ile val ile gin lys arg his asn thr arg leu leu arg arg met glu lys asp lys

2581/861 2611/871
CCA GTG GTC AAT AAA GAT CTT ACT CCT GCT GAA ACA GAT GTC GCT GTT GCT GCT GTT AAA
pro val val asn lys asp leu thr pro ala glu thr asp val ala val ala val lys

2641/881 2671/891
CAA TGG GAG GAG GAT ATG AAA GAA AGC AAA GAA ACT GGA ATT GTG AAC CCA TCA TCC GGA
glu trp glu glu asp met lys glu ser lys glu thr gly ile val asn pro ser ser gly

2701/901 2731/911
ACA ACT GTG GAT AAA CTT ATC GTT TCG AAA TAC AAA TTC GAT TTT TTC TTG GCA TCT CAT
thr thr val asp lys leu ile val ser lys tyr lys phe asp phe phe leu ala ser his

2761/921 2791/931
CAT GGT GTC CTT GGT ACA TCT CGT CCA GGA CAT TAC ACT GTT ATG TAT GAC GAT AAA GGA
his gly val leu gly thr ser arg pro gly his tyr thr val met tyr asp asp lys gly

2821/941 2851/951
ATG AGC CAA GAT GAA GTC TAT AAA ATG ACC TAC GGA CTT GCT TTT CTC TCT GCT AGA TGT
met ser gln asp glu val tyr lys met thr tyr gly leu ala phe leu ser ala arg cys

2881/961 2911/971
CGA AAA CCC ATC TCG TTG CCT GTT CCG GTT CAT TAT GCT CAT TTA TCA TGT GAA AAA GCG
arg lys pro ile ser leu pro val pro val his tyr ala his leu ser cys glu lys ala

2941/981 2971/991
AAA GAG CTT TAT CGA ACT TAC AAG GAA CAT TAC ATC GGT GAC TAT GCA CAG CCA CGG ACT
lys glu leu tyr arg thr tyr lys glu his tyr ile gly asp tyr ala gln pro arg thr

3001/1001 3031/1011
CGA CAC GAA ATG GAA CAT TTT CTC CAA ACT AAC GTG AAG TAC CCT GGA ATG TCG TTC GCA
arg his glu met glu his phe leu gln thr asn val lys tyr pro gly met ser phe ala

3061/1021 3091/1031
TAA CAT TTT GCA AAA GTG TCG CCC GTT TCA ATC AAA TTT TTC AAT TGT AGA TAT TGT ACT
OCH (SEQ ID NO: 3)

3121/1041 3151/1051
TAC TTT TTT TTA AAG CCC GGT TTC AAA AAT TCA TTC CAT GAC TAA CGT TTT CAT AAA TTA

3181/1061
CTT GAA ATT TAA AAA AAA AAA AAA (SEQ ID NO: 2)

Figure 7

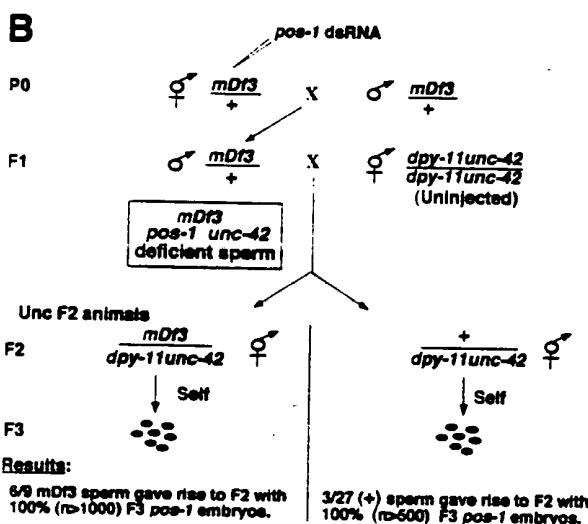
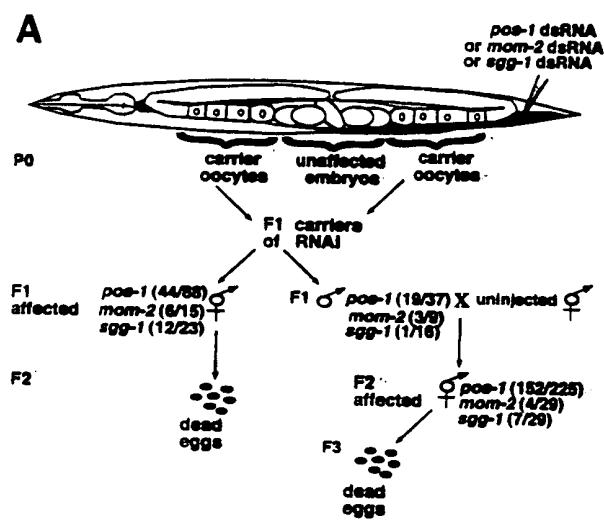


Figure 8

A	Injected P0	F1
♀	<u>rde-1 unc-42</u> + pos-1 dsRNA	<u>self X</u> rde-1 (-) 11/24 rde-1 (+) 9/72
♀	<u>rde-2 unc-13</u> + pos-1 dsRNA	<u>self X</u> rde-2 (-) 0/39 rde-2 (+) 23/78
♀	<u>mut-7 dpy-17</u> + pos-1 dsRNA	<u>self X</u> mut-7 (-) 0/15 mut-7 (+) 20/50
♀	<u>rde-4 unc-69</u> + pos-1 dsRNA	<u>self X</u> rde-4 (-) 5/15 rde-4 (+) 11/48

B	P0	Injected F1
♀	<u>rde-1 unc-42</u> + pos-1 dsRNA	<u>self X</u> rde-1 unc-42 0/37 rde-1 unc-42 0/37
♀	<u>rde-4 unc-69</u> + pos-1 dsRNA	<u>self X</u> rde-4 unc-69 0/37 rde-4 unc-69 0/37

Figure 9

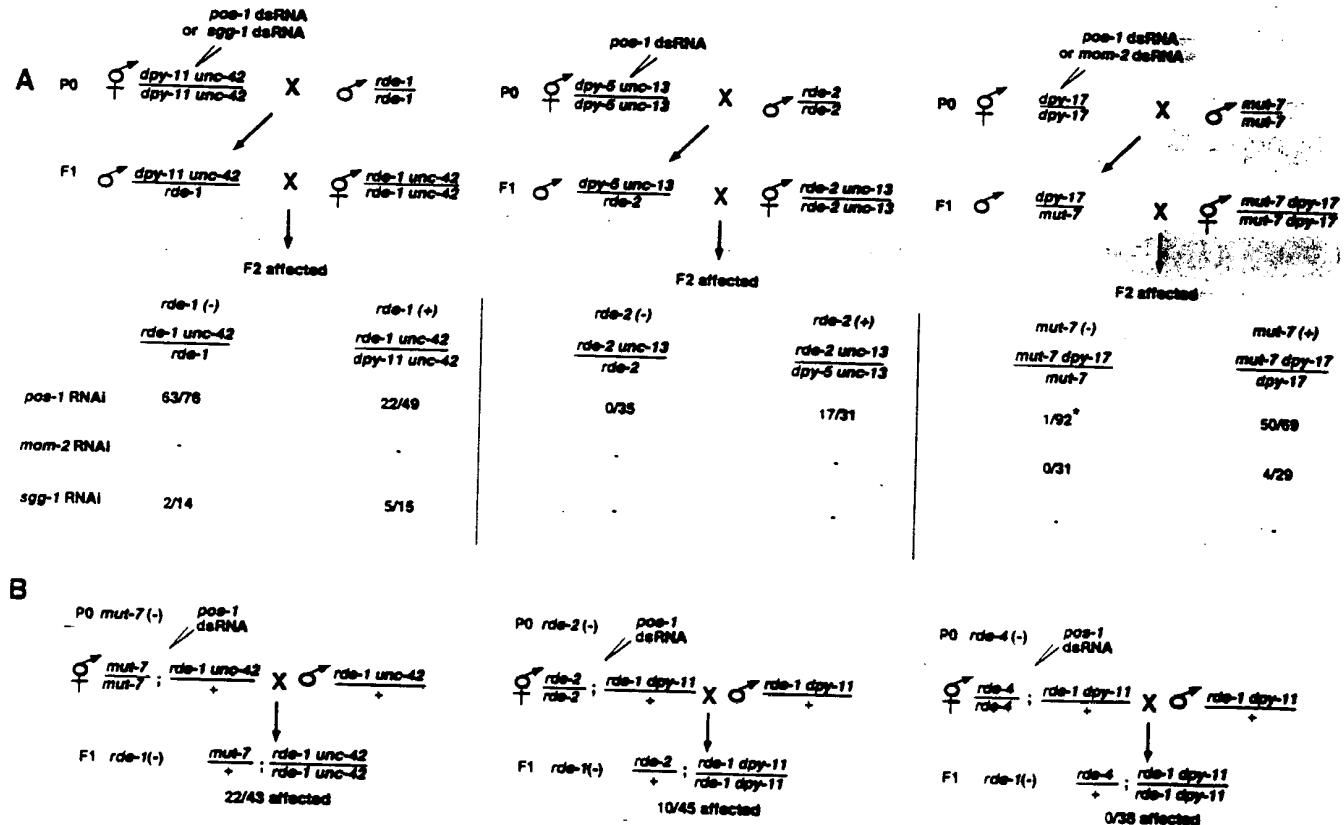


Figure 10A

10 20 30 40 50 60
ATGGATTAAACCAAACTAACGTTGAAAGCGTTTCGGTGGATCAGATGTTCTATGAAG
M D L T K L T F E S V F G G S D V P M K

70 80 90 100 110 120
CCTTCCCGATCGGAGGATAACAAAACGCCAAGAAACAGAACAGATTGGAGATGTTCTG
P S R S E D N K T P R N R T D L E M F L

130 140 150 160 170 180
AAGAAAAACTCCCCCATGGTACTAGAAGAGGCTGCTAAGGCTGTCTATCAAAAGACGCCA
K K T P L M V L E E A A K A V Y Q K T P

190 200 210 220 230 240
ACTTGGGCACTGTCGAACCTCTGAAGGCTTCGAGATGACGTTGATTCTGAATGAAATT
T W G T V E L P E G F E M T L I L N E I

250 260 270 280 290 300
ACTGTAAAAGGCCAGCAACAAGCAAGAAAGCTGCGAGACAAAAGGCTGCTGTTGAATAT
T V K G Q A T S K K A A R Q K A A V E Y

310 320 330 340 350 360
TTACGCAAGGTTGTGAGAAAGGAAAGCACGAAATCTTTTCATTCCTGGAACAAACCAA
L R K V V E K G K H E I F F I P G T T K

370 380 390 400 410 420
GAAGAAGCTCTTCGAATATTGATAAAATATCGGATAAGGCTGAGGAATTGAAACGATCA
E E A L S N I D Q I S D K A E E L K R S

430 440 450 460 470 480
ACTTCAGATGCTGTTCAAGGATAACGATAACGATGATTGATTCTACAAGTGCTGAATT
T S D A V Q D N D N D D S I P T S A E F

490 500 510 520 530 540
CCACCTGGTATTCGCCAACCGAGAATTGGCTGGAAAGTTGCAGGAAAAATCTCAAAAA
P P G I S P T E N W V G K L Q E K S Q K

550 560 570 580 590 600
AGCAAGCTGCAAGCCCCAATCTATGAAGATTCCAAGAAATGAGAGAACCGAGCGTTCTTG
S K L Q A P I Y E D S K N E R T E R F L

610 620 630 640 650 660
GTTATATGCACGATGTCAATCAAAAACCAAGAGGAATCAGAAGTAAGAAGAACGGACGCA
V I C T M C N Q K T R G I R S K K K D A

670 680 690 700 710 720
AAGAATCTTCAGCATGGTTGATGTGAAAGCGTTGGAAAGACGGTATCGAATCTCTGGAA
K N L A A W L M W K A L E D G I E S L E

730 740 750 760 770 780
TCATATGATATGGTTGATGTGATTGAAAATTGGAAAGAACGCTGAACATTACTCGAAATT
S Y D M V D V I E N L E E A E H L L E I

Figure 10B

790 800 810 820 830 840
CAGGATCAAGCATCCAAGATTAAAGACAAGCATTCCGCACTGATTGATATACTCTCGGAC
Q D Q A S K I K D K H S A L I D I L S D

850 860 870 880 890 900
AAGAAAAAGATTTTCAGACTACAGCATGGATTTCACAGTATTATCAGTGAGGCACAATGGGA
K K R F S D Y S M D F N V L S V S T M G

910 920 930 940 950 960
ATACATCAGGTGCTATTGGAAATCTCGTTCGGCGCTAGTTCTCCAGACCCCCGACGAT
I H Q V L L E I S F R R L V S P D P D D

970 980 990 1000 1010 1020
TTGGAAATGGGAGCAGAACACACCCAGACTGAAGAAATTATGAAGGCTACTGCCGAGAAG
L E M G A E H T Q T E E I M K A T A E K

1030 1040 1050 1060 1070 1080
GAAAAGCTACGGAAGAAGAACATGCCAGATTCCGGGCCCTAGTGTTTGCTGGACATGGT
E K L R K K N M P D S G P L V F A G H G

1090 1100 1110 1120 1130 1140
TCATCGGCGGAAGAGGGCTAACACAGTGTGCTTGTAAATCGGCGATTATCCATTCAACACC
S S A E E A K Q C A C K S A I I H F N T

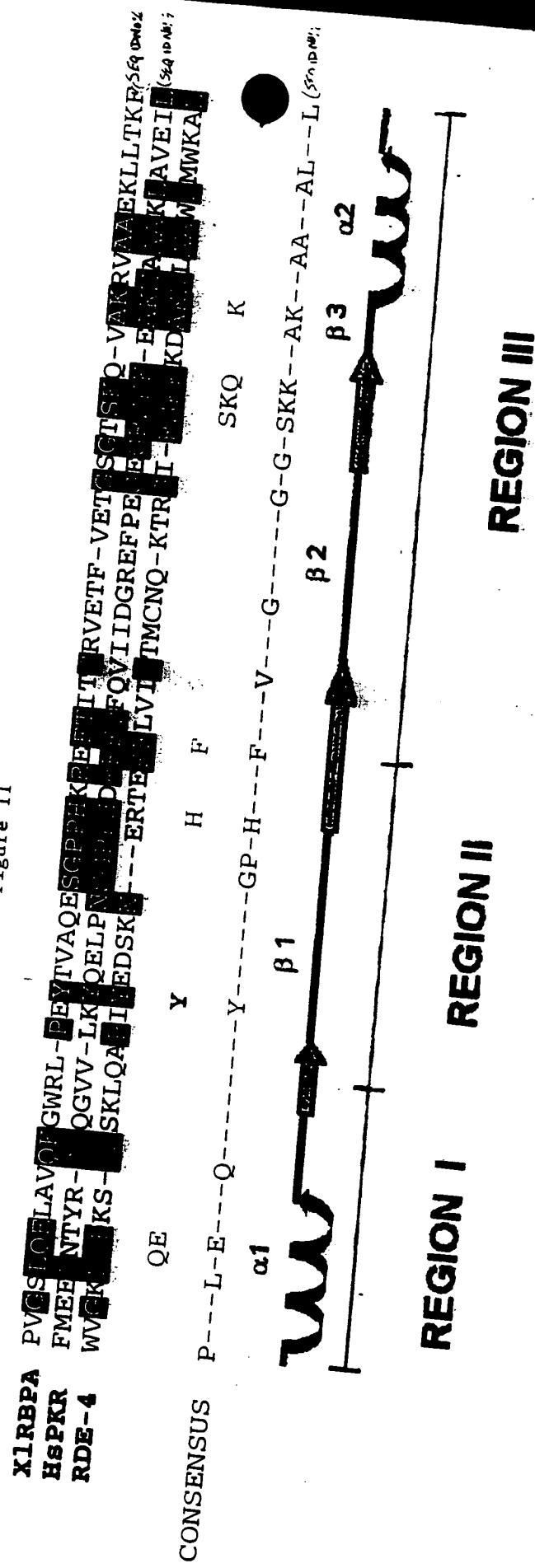
1150 1160 1170 1180 1190 1200
TATGATTTCACGGATTGAAAATATTATTGCGTATTCTGAAAAATGAAGCGCTGAAATGA
Y D F T D * K Y Y C V F L K N E A S E *

1210 1220 1230
TTATAAAAAAAAAAAAAAA (SEQ ID NO:4)
L * K K K K K (SEQ ID NO:5)

DIGESTION BY PROTEINASE K

PREGRESO DE LA TECNOLOGIA

Figure 11



Rescue of *rde-4*:

Figure 12

